us-10-800-161-28.rge

Title: Perfect score:

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AC14723 Pan trogl
AC14729 Pan trogl
BC192936 Plasmodiu
BC058827 Homo sapi
AL513166 Human DNA
BV208515 FYE_225
AC130873 Rattus no
AC131170 Rattus no
AC131170 Rattus no
AC131170 Rattus no
AC131170 Rattus no
BX248236 Zebrafísh
CQ681076 Sequence
AC130614 Rattus no
AC130614 Rattus no
AC130617 Mouse DNA
AC108584 Homo sapi
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AC39257 Homo sapi
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AC368307 Homo sapi
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                                                                                                                                                                                                                                                                                                                                              AC092515 Papio anu
AL157900 Homo sapi
AL358434 Human DNA
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1 (bases 1 to 1700)

1 (bases 1 to 1700)

Arabidopsis gene encoding a protein involved in the regulation of the gene encoding a protein involved in the regulation of the gene expression in plants

Patent: US 6706552-A 3 16-MAR-2004;

Syngenta Participations AG; Basel;
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Pred. No. 1.4e-51;
0; Mismatches 1;
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CQ691076
AL64556
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BX957291
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Best Local Similarity 99.6%;
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       254920
276137
174887
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CS025770 Sequence
AR488146 Sequence
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AC008964 Homo sapi
AC073652 Homo sapi
AC073528 Homo sapi
AC073528 Homo sapi
AC06558 Homo sapi
AC00558 Homo sapi
AC008563 Homo sapi
AXX09879 Sequence
BC01775 Homo sapi
                                                                                                                       (without alignments)
6762.964 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                          time 2303 Seconds
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                       GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                         January 11, 2006, 23:58:55; Search
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Maximum Match 100%
Listing first 45 summaries
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                                                                              nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180

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Sequence Homo sapi Homo sapi

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Direct Submission

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Institute, Department of Plant Gene Research; 1532-3, Yana, Kisaraau, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3955, Fax:81-438-52-394)

Address for correspondence: kaos@kazusa.or.jp

Por the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MFEII Genes with similarity to proteins in the databases are described in product or note qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-13/),

GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/gervicee/NetGene2/) and SplicePredictor (Volker Brende), Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K9122 and the 3' clone is MJL14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty
                                                                                                                                                                                                                                                       PLN 14-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
2 (bases 1 to 83650)
Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S.
Direct Submission
                                                                                                                                                                                               83650 bp DNA linear PLN 14-FBB-2
AB023041 BA000014
AB023041.1 GI:4220640
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join(1705. 2463,2848. 2739,2862. 2949,3037. 3107,
3190. 3273,3410. 3514)
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complement (542. .764)
/note="CDS is reported in Acc# AP000599
contains similarity to CHP-rich zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
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                                                    TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                               818 TTGACTAAACGTTAAACGCCGTTAACATTTTC 851
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Arabidopsis thaliana
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DNA Res. 7 (2), 131-135 (2000)
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|number=1
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AUTHORS
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complement (join(10090. .10408,10649. .10804,10916. .10962))
/note="unnamed protein product, gene_id:MPE11.3
similar to unknown protein
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AVSLIKNPELIKRYHMEYLEAGADIVVTSSYQATIPGFLSRGLSIEESESLLÇKSVEL
AVBADDRFWEKVSKVSGHSYRRALVARSIGSYGATLADGSEYSGHYGENVSLDKKDF
HRRRLQVIVBAGGGLAFETIPMKLEAQACVELLEEEKVQIPAWICTSYDGSKAPSG
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                                                                                                                    /translation="wyvrskirrienempalsstwiteckivswiktegeklakgesvvvv
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TGPFGRITASDPVETSBAPATAQPAPVATAGATTTVILPPLLPDSSIVPFTA
MQSAVSKNMIESLSVPFFRVGYPVNTDALDALYEKVKPKGVTMTALLAKAAGMALAQH
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PPSCEETVTELVRASSDSSEVGELCGFEDHVTEFGFCDLGDDGLFEYFDGCLDSGDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="mmepkakydrolmytioctleeasiclinggpigsnalknivig
gvgsitivegskvligdiwkophrhaleokpsisegprdenntvforreohsvporol
eonriagotvrpmdiarriwasigrmwsladprttygkearaitdpppgrvlarlisl
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/tanalation="MNNSLKKEREVEEDNGKSDGNRGKPSTEVVRTVTEEVDEFFKI
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FVVNDPYATDYSSSEEERRSQRRKRYVCEIDLPFAQAATQAESESSYCQESNNNGVSK
TKISACSKKVLRSKASPVVGRSSTTVSKPVGVRQRKMGKWAABIRHPITKVRTWLGTY
                                                                                                                                                                                                                                                                                PVVAASCKDGKSFSYNSSINIAVAVAINGGLITPVLQDADKLDLYLLSQKWKELVGKA
RSKQLQPHBYNSGTFTLSNLGMFGVDRFDAILPPGQGAIMAVGASKPTVVADKDGFFS
VKNTMLVNVTADHRIVYGADLAAFLQTFAKIIENPDSLTL"
complement (4594. , 5106)
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product="AP2_domain_transcription factor-like protein"
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/note="unnamed protein product; gene_id:MPE11.4
unknown protein"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown protein"
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PAT 11-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfitzner, A. and Roth, B. Chemically-inducible promoters for the expression of proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1147 GACGGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GACGGCTATAAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                         GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                 CAATCTCCACCGTCCAATTTAATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%; Score 258.4; DB 6; 99.6%; Pred. No. 2.2e-48; ive 0; Mismatches 1;
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Sequence 2 from Patent WO2005014829.
CS025770.
CS025770.1 GI:60496427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis tha.
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatent: EP 1502953-A 2 02-FEB-2005;
Universitaet Hohenheim (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         CS007929 1226 bp
Sequence 2 from Patent EP1502953.
CS007929
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Best Local Similarity 99.6
Matches 259; Conservative
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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CS025770
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CS007929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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36797. .36871) 
/note="unnamed protein product; contains similarity to 
transcription-associated zinc ribbon protein 
gene_id:MPEII.II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MATPLSISSNPLTSRHCYRLHLSSTSFKGNVSVLGANPSQILSL
KLNQTLKTRNQQQFARPLVVVSQTAATSSAVVAPERERLDNLGPQFGSRKQKRKGRG
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VNIKDIETAGFGBDSVSLETLKQKGIJNPSGRERKLPLKILGTGELSMKLTFRARAF
STQAKEKLEASGCTLTVLPGRKKWVKPSVAKNQARADEYFAKGRAAARAATSEPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MEKSRESEFLFCNLCGTMLVLKSTKYAECPHCKTTRNAKDIDK
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QTTYYTCPNCAHRFTEG"
Join (37285. . . 37965, 38579. . . 38674)
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                                                                                    /evidence=not_experimental
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VCMEHPHNGTLLICSSYENGCRPYMCDTSHRHSNCPDOPRKASKEKPSLSLLAREEES
NEPTEMEDVISLICSSYAVALLGBAAASITVVDLSDGRRGEEEVEEEEEVVVEEEEESIV
YTEPDOBEKNKPQKTCPLCGHIKSWVVVKAARCFWNSKHRSCSCETCDPSGSYSDLR
KHARLLHPGVRPSEADPERQRSWRRLERQSDLGDLLSTLQSSPGGDEISNDGFLPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLLTVYFLIRVPRPESSGSRSSSWSGTSRARTHTSGRRRSSRPASLWGESYEGNTGT
SPRDEENNGSSDEQVSGTRRRSRRRTVIDDDDEEEEP"
complement (join (32197. .32430, 32525. .32676, 32969. .33332,
33404. .33487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join(33961. .34021,34114. .34226,34391. .34482,34602. .34800))
/note="unnamed protein product; gb|AAF26483.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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unknown protein"
                                                                                                                                                                                                 30765. .31883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272.4; DB 15; Length
Pred. No. 5.8e-52;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                      gene id:MPE11.8
similar to unknown protein"
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Best Local Similarity 99.6
Matches 273; Conservative
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1206

DEFINITION ACCESSION VERSION KEYWORDS

12103 TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA 12044

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61 ATAAAGTGTGACGTCATGATACTTAACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120

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PLN 09-SEP-2004

Arabidopsis thaliana (thale cress)

ORGANISM

SOURCE

REFERENCE AUTHORS

source

ORIGIN

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FEATURES

JOURNAL

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Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohayama, K., Kobayama, M., Toyoda, A., Sakaki, Y., Sakurai, T., Ilda, K., Kawai, Y., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Carninci, P., Direct Submission

Submitted (16-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@ge.riken.jp,
Pax:81-45-503-9585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with Bamki and XhoI was ligated to modified Lambda FLC-1E vector (Carninci et al. (2001) Genomics 77:79-90) digested with Bamki and Sali. This clone is in a modified pBluescript vector.

Please visit our web site (http://rarge.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="winnslikkeerveedingkedgerkertevrtyteeevdefkt
LRRVHVATRTVAKVNGGVAEGELPSKKRKRSQNLGLRNSLDCNGVRDGEFDEINRVGL
QGLGLDLNCKTEPDSVSLSL"
                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Seki,W., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoco,N., Oishi,K.,
Koharara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs
Unpublished
2 (bases 1 to 544)
                                                                                                                                                                                                                                                                                               Eukaryofa; Viridiplantae; Straptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                               AK175239 544 bp mRNA linear PLN 09-
Arabidopsis thaliana mRNA for NIMIN-2, complete cds, clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 AGCAAATAATTTTTTCTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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18.2%; Score 50; DB 15; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 50; Conservative 0; Mismatches 0; Indels

    .544
    /organism="Arabidopsis thaliana"

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                                                                                                                                                                                      AK175239.1 GI:51968619
EL CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone="RAFL21-66-M11"
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                                                                                                                                      RAFL21-66-M11.
                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                            ORGANISM
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JOURNAL
REFERENCE
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JOURNAL
                      RESULT 6
AK175239
LOCUS
                                                                                                                                                               ACCESSION
                                                                                                                                                                                            VERSION
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Arabidopsis thaliana
Evkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis gene encoding a protein involved in the regulation of SAR gene expression in plants
Patent: US 6706952-A 1 16-MAR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                      Pfitzner, A. and Roth, B. Chemically-inducible promoters for the expression of proteins in
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                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Universitaet Hohenheim (DE)
Location/Qualifiers
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Sequence 1 from patent US 6706952.
AR488146
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/organism="unknown"
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Cad, R.M. and Dietrich, R.A.
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Matches 259; Conservative
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                                                       PRI 08-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                           Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (28-ARR-2001) DOE Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 94598, USA
4 (Dases 1 to 14384)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
Submitted Walnut Creek, CA 94598, USA
(bases 1 to 143841)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (08-JUN-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13876485.

Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                          ACO08964 143841 bp DNA linear PRI 08-JUN-
Homo sapiens chromosome 5 clone CTD-2360A17, complete sequence.
ACO08964
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OB Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Estimated Total Number of Errors is 0.1.
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1. 143841
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                    2 (bases 1 to 143841)
DOE Joint Genome Institute.
                                                                                                            AC008964.6 GI:14329064
                                                                                                                                               Homo sapiens (human)
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Matches 85; Conserva
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Homo sapiens chromosome 12 clone RP11-148D15, WORKING DRAFT
SEQUENCE.
                  PRI 31-JUL-2001
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (31-701-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 31, 2001 this sequence version replaced gi:13677000.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 195931)

DOB Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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1 (bases 1 to 167034)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
AC010633 195931 bp DNA linear PRI 31-JUL
Homo sapiens chromosome 5 clone CTD-2317K6, complete sequence.
AC010633
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Best Local Similarity 56.3%; Pred. No. 1;
Matches 85; Conservative 0; Mismatches 66; Indels 0;
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.4.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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/clone="CTD-2317K6"
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DOE Joint Genome Institute.
Direct Submission
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Alebrooke, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Banger, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, B. Bryant, N.P., Bhay, C., Bowie, P., Burket, C., Blankenburg, K. B., Bryant, N.P., Bhay, C., Bowie, S., Brieva, M., Brown, M. Bryant, N.P., Bhay, C., Bowie, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Claveland, C. D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M. L., Davis, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Derper, H., Dougan-Recha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Erotto, M., Falls, T., Perraguto, D., Flago, N., Ford, J., Foster, P., Frantz, P., Gorrell, H.H., Havlak, P., Hawes, A., Harnandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hame, J., Jackson, L.E., Jacobson, B., Jis, Y., Johnson, R., Holloway, C., Hollins, B., Homei, P., Howard, S., Hune, J., Jackson, L.E., Jacobson, B., Jis, Y., Johnson, R., Havlak, P., Hume, J., Jackson, L.E., Jacobson, B., Jis, Y., Johnson, R., Havlak, P., Hane, J., Ludar, M., Maheshwari, M., Maheshwari, M., Mabeshwari, M., Mabeshwari, M., Mabeshwari, M., Mabeshwari, M., Mattin, R., Martindale, A., Matcher, M., Martin, R., Martin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
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Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Mammalia; Eutheria; Eutheria; Eurchontoglires; Primates; Catarrhini; Mammalia; Eutheria; E
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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16.1%; Score 44.2; DB 14; Length 167034;
Best Local Similarity 51.2%; Pred. No. 2;
Matches 103; Conservative 0; Mismatches 98; Indels 0; (
                                                                                                                                                 1 167034: contig of 167034 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DN
/db_xref="taxon:9606"
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Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metsker, M., Miller, A., Miner, G., Miner, G., Miner, G., Miner, T., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newtson, T., Newtson, N., Oguh, M., Okwonn, G., Oragunye, N., Ovickerson, E., Nwokenkwo, S., Oguh, M., Okwonn, G., Peter, L., Pickens, R., Pace, M., Paycon, B., Peter, J., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saery, G., Scherer, S., Scott, G., Sham, C., Shooshtaria, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, F., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Wasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Wall, R., Wall
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(bases 1 to 167041) Unpublished

Worley, K.C.

Direct Submission
Submitted (22-UTN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Saylor Plaza, Houston, TX 77030, USA
(Passes 1 to 167041)

Direct Submission

REFERENCE AUTHORS TITLE JOURNAL

Submitted (01-MAY-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 1, 2001 this sequence version replaced gi:13876431.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html

--- Summary Statistics ------

167603 166580 3.9018-06 0.000210109 0	Edited+Context										*	0 35 40							- DO B D CO C B B D D "	clone AC068800"																					
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Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tasfarye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M., Direct Submission.

Lu bubmitted (01-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7144995.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 205676; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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8: contig of 212 bp in length
8: gap of 100 bp
7: contig of 4944 bp in length
8: gap of 100 br
9: gap of 100 br
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of 1476 bp in length
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Web site: http://www-seq.wi.mit.edu
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                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                           COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74249 ATTATACAAATATACACATAAGAAATTGATTCTAAATAAGCAATATAACATCACATTTG 74190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74189 AATTGATTTTAACCAACTACACTATTCAGTGTAATATGTGGCAGGAACATTTATAAAG 74130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC024628 207976 bp DNA linear HTG 25-MAY-2000 Homo sapiens chromosome 12 clone RP11-632011 map 12, WORKING DRAFT SEQUENCE, 24 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 ATGTCATTAGCATCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTC 167
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 ATTCCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TAAGTTCCACACGCGCGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 167041;
                                                                                                                                                                                                                                                                                                                                                                                                                                       98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 207976)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 12, clone RP11-632011
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Sco...
51.2%; Pred. No. z,
... 0; Mismatches
                                                                                                       /rpt_family="MIR"
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11288. .11321
                                                                                                                                                                                                                                                                                                             complement (12398. .12636)
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complement (12641. .13107)
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complement(8256. .8962)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC024628.3 GI:8076668
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                              'rpt family="MLT1G"
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Best Local Similarity
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TITLE
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AC024628
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셤 ð 유 à g ð estimated_length=100

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197 88196: Garing of 11782 bp in length 197 88296: gap of 100 bp 120765: contig of 13769 bp in length 1666 102165: gap of 100 bp 1666 102165: gap of 100 bp 1670: contig of 14205 bp in length 1371 116470: contig of 100 bp 171781: contig of 38172 bp in length 17189: contig of 38172 bp in length 17189: contig of 3807 bp in length 1700 207976: contig of 36087 bp in length.
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4: contig of 10594 bp in length
4: gap of 100 bp
5: contig of 11782 bp in length
5: gap of 100 bp
6: contig of 100 bp
7: contig of 13769 bp in length
7: gap of 100 bp
of 10290 bp in length
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11032. 1131
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11132. 12855
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gap of J
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171790
171890
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76415
88197
88297
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gap

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Hominidae, Homo.

Hominidae, Homon.

Hominidae, Homon.

Hominidae, Homini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC005158 266344 bp DNA linear PRI 30-JAN-2004
Homo sapiens BAC clone GSI-250N6 from 7, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 ATTCCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATG 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 TAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.2%; Pred. No. 1.9;
Matches 103; Conservative 0; Mismatches 98; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AAATAATTTTTTTGACTAA 248
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                                                                     4813. .34912
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AC005158
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19857. .20139
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20140. .20482
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Submitted (30-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 25, 2001 this sequence version replaced gi:5091650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 266344)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
8 (bases 1 to 266344)
                                                                                                                                                                                                                                                                                                                                                          Submitted (20-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (Bess 1 to 266344)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to assiste all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
              Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Furey, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Flicek, P., Chinwalla, A.T., Gish, W.B., Eddy, S.R., McPherson, J.D., Olson, W.V., Bichler, B.E., Green, E.D., Waterscon, R.H. and Wilson, R.K. The DNA sequence of human chromosome 7
faugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                            2 (bases 1 to 266344)
Bauer, C., McPherson, C. and Williams, D.
The sequence of Homo sapiens BAC clone GSI-250N6
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_GS250N06
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                                                                                                                                                                                                                                                                                          3 (bases 1 to 266344) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (bases 1 to 266344)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                           Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

TITLE

REFERENCE AUTHORS

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the

MAPPING INFORMATION: restriction digest.

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Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information boout the map position of this sequence, see the map position of this sequence, see they://www.nigri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu
                                                                                                                                                                                                 This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com).
Cell line: lymphoblastoid
Haplotypes: two
                                                                                                                                                                                                                                                                                                                                                                                                                                   Actual start of this clone is at base position 1 of GS1-250N6 actual end is at base position 266144 of GS1-250N6. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="GA-rich"
23875. .24166
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25208. .25431
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28192. .28253
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23398. .23447
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Consensus quality: 8918 bases at least Q40
Consensus quality: 93760 bases at least Q30
Estimated insert size: 94635; sum-of-contigs estimation
Estimated insert size: 94635; sum-of-contigs estimation
Quality coverage: 5.84 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72000 AGTCCTAATACAAGATTAAATAATTTTAGATGGTGATATAATTTTTCAAAAGTAACC 72059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72060 AATGCTGGGGTTATTAAGAATTCGATTTAGTTACTGACAAGGTGATATTATTATTATGTACTG 72119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced

* This sequence all be replaced

* the finished sequence as soon as it is available and

* the accession number will be preserved.

* 34594: contig of 34594 bp in length

* 34695 5143: contig of 1649 bp in length

* 5144 66435: contig of 15182 bp in length

* 51244 66435: contig of 15182 bp in length

* 6525: agap of unknown length

* 6526: contig of 5841 bp in length

* 72367 72466: gap of unknown length

* 72467 79529: contig of 7163 bp in length

* 79630 80679: contig of 7163 bp in length

* 80780 94703: contig of 950 bp in length

* 10cation/Qualifiers
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/estimated_length=unknown
51144. .51243
/estimated_length=unknown
66426. .66225
/estimated_length=unknown
72367. .72466
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80680. .80779
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                                                                                                                                               Center Project Name: 391027, H433
Center clone name: CIT-HSPC_536A23

    94703
    /organism="Homo sapiens"

                                                                       Web site: http://www.jgi.doe.gov
                  Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DN/db_xref="taxon:9606"
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-----Genome Center
                                                                                                                          Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162912 AGCATAGTTTAGTAGAAAGAATAATATCATTACAGAATGAAATTCTAATGTCAAAATA 162971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162972 ATTTCTTAAAAGGATTCCACAAAATGAAAACATAATAATCCGGCTTGAAAAACCTCATT 163031
                                                                                                                                                                                                                                                                                                                                                                                                                              /produčt="unknown"
/protein_id="AAS02015.1"
/db_xref="G1:41393490"
/tanslation="NEAQSHSSTTTEKKKVENSIVKCSTRTDVSEKAVASSTTSNEDE
SPGOTYTRERRNATINGPQNVQGLSKVSEEPSTSSDERASLIKKEIHGSLPHVAEPSV
PYRGTVFAMDPRNGYMEPHY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC008563 94703 bp DNA linear HTG 18-JUL-2000 Homo sapiens chromosome 5 clone CTC-536A23, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7708951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 CTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCACAATCTCCACCGTCCAATTTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 94703)

20 Joint Genome Institute.

Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                 /note="Homo sapiens GLI-Kruppel family member GLI3 (Greig
cephalopolysyndactyly syndrome) (GLI3), mRNA.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 TITAGIIGIIGACAAIAICGACCGICIAAGIICCACACCGACGGCIATAAGAGIIICAII 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 AATTITICCACACATGGACTICCTITATICCAAAAGTCAATAAAGTGTGACGTCATGATA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                    complement (join (<30701. .30943,105605. .105728))
/gene="GLI3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
15.8%; Score 43.4; DB 8; Length 266344;
Best Local Similarity 50.2%; Pred. No. 2.7;
Matches 107; Conservative 0; Mismatches 106; Indels 0;
                                                                                                                                                               complement(join(30701. .30943,105605. .105771))
/gene="GLI3"
                                                                                                                                                                                                                                                                                                                                      H GS250N06.1
This gene was based on gi (13518031)
Continues as H GS489L14.1"
/codon_start=1
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                                                     /rpt_family="MIR"
30611. .30652
/rpt_family="(CA)n"
complement(30701. .105771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TTTTG)n"
34931. .34953
/rpt_family="(TCTCCC)n"
36317. .36368
/rpt_family="GA-rich"
28282. .28508
/rpt_family="MIR"
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HTG; HTGS PHASE2; HTGS DRAFT.
HOMO Sapiens (human)
HOMO Sapiens
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DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                       /gene="GLI3
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AUTHORS
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Karzyninski, M.I., Skallska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: m Column: 7.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 GACTÁTAACAGAAATCATÁTTTAATATATAAATTAATACTTCAAATATCTTTCACATT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R. Direct Submission Direct Submission Mammalian Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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24:
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    organism="Homo sapiens"

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/clone_lib="NIH_MGC_77"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:4692106"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heiseh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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           TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACGGGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Algate, P.A. and Mannion, J. Compositions and methods for the therapy and diagnosis of ovarian
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                      184 GGCTATAAGAGTTTCATTATAAATTTTAGCAAATAAAATCAGCAAATAATTTTTTTGTTG
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Sequence 1719 from Patent WO0157207.
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Best Local Similarity 57.73
Matches 75; Conservative
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8 셤 ò 셤 ò 셤 ö 183 416 Sequence 69, Appl Sequence 2, Appli Sequence 10963, A Sequence 2117, Ap

US-10-312-841-2 US-10-282-122A-10963 US-10-029-386-2117

US-10-275-762-69 US-10-810-788A-6

Sequence 147689, Sequence 147689, Sequence 147689, Sequence 147689, Sequence 534423, Sequence 7701, Ap Sequence 7701, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 585231, Sequence 585231,

US-10-311-455-26 US-10-027-632-147687 US-10-027-632-147688 US-10-027-632-147689 US-10-027-632-147689 US-10-027-632-147689 US-10-027-632-147689 US-10-027-632-147689 US-10-027-632-147689 US-10-147-603-1 US-09-925-065A-534423 US-10-085-783A-7701 US-09-913-356-2 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-09-913-356-3 US-10-913-356-3

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1 TCTAGAAATATAGCCGATACCAATTTTTCCACATGGACTTCCTTTATTCCAAAGTCA
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Sequence 28, Application US/10800161
Sequence 28, Application US/10800161
Sequence 28, Application US/10800161
Sequence 28, Application US/10800161
SEQUENCE 28, SEQUENCE 28, SEQUENCE 28, SEQUENCE 28, SEQUENCE 29, SEQUENCE 31080CPL
CURRENT FILING DATE: 2004-03-12
CURRENT FILING DATE: 1999-12-15
PRIOR FILING DATE: 2000-01-11
SUMBER OF SEQ ID NOS: 31
SEQUENCE 28, SEQ ID NOS: 31
SEQUENCE 28, SEQ ID NOS: 31
SEQUENCE 28, SEQ ID NOS: 31
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ORGANISM: Arabidopsis thaliana
14.4 375 3

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Sequence 676, App
Sequence 1719, Ap
Sequence 6, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 36002, A
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Sequence 24, Appl
Sequence 3, Appli
Sequence 1, Appli
Sequence 102510,
Sequence 102510,
Sequence 102511,
Sequence 102511,
Sequence 102511,
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Sequence 102511,
Sequence 102511,
                                                                                                         ; Search time 812 Seconds (without alignments) 2790.406 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq: *

2: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq: *

3: /cgn2 6/ptodata/1/pubpna/USO8A PUBCOMB.seq: *

4: /cgn2 6/ptodata/1/pubpna/USO8B PUBCOMB.seq: *

5: /cgn2 6/ptodata/1/pubpna/USIO8 PUBCOMB.seq: *

6: /cgn2 6/ptodata/1/pubpna/USIO8 PUBCOMB.seq: *

7: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *

8: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *

7: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *

8: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *

9: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *

10: /cgn2 6/ptodata/1/pubpna/USIOB PUBCOMB.seq: *
                      GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-800-161-26
US-10-800-161-27
US-10-800-161-27
US-10-800-161-24
US-10-800-161-3
US-10-800-161-3
US-10-800-161-3
US-10-800-161-3
US-10-800-161-1
US-10-027-632-102510
US-10-027-632-102510
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US-10-101-510-542
US-10-242-535A-36002
US-10-085-783A-36002
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                                                                                                                                                                                                                                                                               9793542 seqs, 4134689005 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 using sw model
                                                                                                              January 12, 2006, 00:23:59
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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100.0%; Score 274; DB 7; Length 274; 100.0%; Pred. No. 8.1e-61; ive 0; Mismatches 0; Indels (

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61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
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                                                              Length 544;
                                                                                                       1; Indels
                                                              DB 7;
                                                           Score 272.4; DB 7
Pred. No. 2.7e-60;
0; Mismatches 1
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; Sequence 25, Application US/10800161
; Publication No. US20040154051A1
; GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Dietrich, Robert A
APPLICANT: Lawton, Kay Ann
TITLE OF INVENTION: INDUCIBLE PROMOTERS
FILE REFERENCE: A-31089G(TP1
; CURRENT APPLICATION NUMBER: US/10/800,161
; CURRENT FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/171,008
PRIOR APPLICATION NUMBER: 60/171,008
; PRIOR PILING DATE: 1999-12-15
; PRIOR PILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 25
LENGTH.: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-800-161-25
ORGANISM: Arabidopsis thaliana
                                                              99.4%;
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Matches 273; Conservative
      ; OKGANISM: AE
US-10-800-161-27
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241 TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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GGRURAL INFORMATION:
GREAL INFORMATION:
GREAL INFORMATION:
GREAT INFORMATION:
GREAT INFORMATION:
GREAT INFORMATION:
GREAT INFORMATION:
GREAT INFORMATION:
TITLE OF INVENTION:
INDUCTBLE PROMOTERS:
FILE REFERENCE: A-31089CIP1
CURRENT FILING DATE: 2004-03-12
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENT IN NOS: 31
SOFTWARE: PATENT IN NOS: 31
SOFTWARE: PATENT IN NOS: 31
SOFTWARE: PATENT IN NOS: 31
SOFTWARE: DATE: 1000-111
TYPE: DNA
                                                                                                Publication No. US20040154051A1
Publication No. US20040154051A1
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Lawton, Kay Ann
TITLE OF INVENTION: INDUCIBLE PROMOTERS
FILL REFERENCE: A-31089CIP1
CURRENT APPLICATION NUMBER: US/10/800,161
CURRENT FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-800-161-26
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LENGTH: 274
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ORGANISM: Arabidopsis thaliana
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Pred. No. 3.3e-60;
0; Mismatches 1; Indels 0
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Sequence 3, Application US/10800161
; Bublication No. US20040154051A1
; GENERAL INFORMATION:
; APPLICANT: Cade, Rebecca M
; APPLICANT: Lawton, Kay Ann
; APPLICANT: Lawton, Kay Ann
; TITLE OF INVENTION: INDUCIBLE PROMOTERS
FILE REPERENCE: A-31089CTPI
; CURRENT APPLICATION NUMBER: US/10/800,161
; CURRENT FILING DATE: 2004-03-12
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Lawton, Kay Ann
TILE OF INVENTION: INDUCIBLE PROMOTERS
FILE REPERENCE: A-31089CIP1
CURRENT APPLICATION NUMBER: US/10/800,161
CURRENT PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 962
                                                                   RESULT 5
US-10-800-161-24
i Sequence 24, Application US/10800161
j Publication No. US20040154051A1
GENERAL INPORMATION:
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US-10-800-161-24
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Best Local Similarity 99.6%;
Matches 273; Conservative
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US-10-800-161-3
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181 GACGGCTATAAGAGTTTTCATTATAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 240
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                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (646)..(665)
OTHER INFORMATION: CAMV ASI salicylic acid response element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.4%; Score 272.4; DB 7; Best Local Similarity 99.6%; Pred. No. 4.1e-60; Matches 273; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATI: Cade, Rebecca M
APPLICANT: Cade, Rebecca M
APPLICANT: Dietrich, Robert A
TITLE OF INVENTION: Inducible Promoter Fragment
FILE REPRENCE: A-31089DIV
CURRENT APPLICATION NUMBER: US/10/760,752
CURRENT PILING DATE: 2004-01-20
PRIOR PILING DATE: 2000-12-8
FRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/17,008
PRIOR APPLICATION NUMBER: 60/17,5519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TIGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              818 rigaciaagciraaacgacgccgrraacarric 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: (863)..(1228)

OTHER INFORMATION: NI16 genomic coding region

US-10-800-161-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (757)..(762)
OTHER INFORMATION: HEXAMERAT 4 element
                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (609)..(614)
OTHER INFORMATION: MYCATR22 element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10760752; Publication No. US20040248303A1; GENERAL INFORMATION:
NAME/KEY: misc feature
LOCATION: (365)..(374)
OTHER INFORMATION: TCA1 motif
                                                                                                                                            motif
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (707)..(712)
OTHER INFORMATION: PAL BOX
                                                                                                                      LOCATION: (426)..(435)
OTHER INFORMATION: TCA1
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (757)..(762)
                                                                                             NAME/KEY: misc feature
LOCATION: (426)..(435)
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219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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19.3%; Score 52.8; DB 7; Length 509;
Best Local Similarity 96.4%; Pred. No. 0.0015;
Matches 54; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 52.8; DB 8; Length 509; 96.4%; Pred. No. 0.0015;
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Sequence 1, Application US/10760752

Sequence 1, Application US/10760752

Publication No. US20040248303A1

GENERAL INFORMATION:

APPLICANT: Cade, Rebecca M

APPLICANT: Cade, Rebecca M

TITLE OF INVENTION: Inducible Promoter Fragment
FILE REFERENCE: A-31089DIV

CURRENT FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US/10/760,752

CURRENT FILING DATE: 2000-12-8

PRIOR PILING DATE: 2000-12-8

PRIOR PILING DATE: 2000-12-8

PRIOR PILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 1

LENGTH: 509

LENGTH: 509
                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (68)..(433)
OTHER INFORMATION: gene product NI16
FEATURE:
NAME/KEY: misc_feature
LOCATION: (142)..(147)
OTHER INFORMATION: Sall site
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/171,008
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/175,519
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
PEATURE:
NAME/KEY: CDS
LOCATION: (68)..(433)
OTHER INFORMATION: gene product N116
                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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LOCATION: (344)..(349)
; TOTHER INFORMATION: ECORI site
US-10-760-752-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc feature

LOCATION: (3447...(349)

OTHER INFORMATION: ECORI site
US-10-800-161-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (142)...(147)
OTHER INFORMATION: Sall site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
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99.4%; Score 272.4; DB 8; Length 1700;
Best Local Similarity 99.6%; Pred. No. 4.1e-60;
Matches 273; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (646)..(665)
OTHER INFORMATION: CAMV AS1 salicylic acid response element
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NAME/KEY: misc_feature
LOCATION: (863)...(1228)
COTER INFORMATION: N116 genomic coding region
US-10-760-752-3
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Sequence 1, Application US/10800161
Publication No. US20040154051A1
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Dietrich, Robert A
APPLICANT: Lawton, Kay Ann
TITLE OF INFORTION: INDUCTBLE PROMOTERS
FILE REFERENCE: A-31089CIP1
CURRENT APPLICATION NUMBER: US/10/800,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (757)..(762)
OTHER INFORMATION: HEXAMERAT 4 element
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (609)...(614)
OTHER INFORMATION: MYCATR22 element
FEATURE:
                                                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (426)..(435)
OTHER INFORMATION: TCA1 motif
                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (365)..(374)
OTHER INFORMATION: TCA1 motif
     PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (707)...(712)
OTHER INFORMATION: PAL BOX
                                                                                                      LENGTH: 1700
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US-10-027-632-112106
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ORGANISM: Human
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LENGTH: 2469
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bublication No. US2020198371A1

Fublication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

FRIOR PILING DATE: 2002-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 102510
                                              219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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  Gaps
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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2; Indels
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     Mismatches
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Best Local Similarity 50.2
Matches 107; Conservative
     54; Conservative
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US-10-027-632-102510
       Matches
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2169 AAAATTATCTGAAATATACTTTCCTTATTGAGAATTTCACAAAATTAAGATCTCAAAAAC 2110
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Sequence 112106, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION WUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PELING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

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PRIOR FILING DATE: 1999-09-28

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PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-03-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 102511
LENGTH: 2469
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Matches 107; Conservative
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2169 AAAATTATCTGAAATATACTTTCCTTATTGAGAATTTCACAAAATTAAGATCTCAAAAC 2110
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                                                                                                                                                                                                                          US-10-U27-S23-102511, Application US/10027632

PUBLICACIÓN NO. US2003020407589

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PLING DATE: 2002-04-20

PRIOR PLING DATE: 2000-07-22

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

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Publication No. US20030204075A9
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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Pred. No. 0.74;
0; Mismatches 106; Indels 0
1989 TTATATTTGCCAAAAATAAGAACAGAAGAAAT 1957
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Best Local Similarity 50.2%;
Matches 107; Conservative (
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US-10-027-632-112106
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ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-24
FRIOR PELING DATE: 2000-02-24
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
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FRIOR FILING DATE: 1999-08-08-09
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                                                                                   15.8%; Score 43.4; DB 5; Length 2469; 50.2%; Pred. No. 0.74; cive 0; Mismatches 106; Indels 0
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Matches 107; Conservative
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Best Local Similarity 50.2
Matches 107; Conservative
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; ORGANISM: Human
US-10-027-632-102510
             US-10-027-632-112106
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361 AGCATAGTTTAGTAGAAAAAAATATCATTACAGAATGAAATTCTAATGTCAAAAATA 420
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15.8%; Score 43.4; DB 6; Length 2469;
Best Local Similarity 50.2%; Pred. No. 0.74;
Matches 107; Conservative 0; Mismatches 106; Indels 0
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Search completed: January 12, 2006, 02:31:42 Job time : 817 sec8

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Sequence 1, Application US/11145703

Publication No. US20050260667A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumahov, Ilya
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Sequence 59119, A
Sequence 59119, A
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2599, Ap
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52, Appl
41, Appl
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7677, Ap
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Sequence 1, Appli
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                                                                                                (without alignments) 551.421 Million cell updates/sec
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7/cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-750-185-59119
US-11-124-368-2918
US-11-136-527-818
US-10-240-708-73
US-10-750-185-3722
US-10-750-185-37551
US-10-750-185-37551
US-11-136-527-6695
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US-11-136-527-6695
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US-11-145-703-1
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                                                                                                                                                                                                                                          6038814 seqs, 404674181 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
                                                                                   January 12, 2006, 00:33:06
                                                                                                                                                                                                 IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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13.8 319608
11.9 1082144
11.7 1765
11.6 100000
11.5 3857
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32.6
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32
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31.4
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Perfect score:
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                                                            nucleic
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27493 ggccricrcacartrigicactrarcagrariarcarcartriccaarcagcacacacacacirg 27434
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                                                                                                                                                                                                                                                                               Sequence 107, Application US/11121086

Sequence 107, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TILLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REPRERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SEQ ID NOS: 107

SEQ ID NO 107
                                                                                            2, Appli
36299, A
36299, A
29212, A
29212, A
17, Appl
                                                      17, Appl
64, Appl
                                                                                                                                                  36704, A
                                                                                                                                                                                                       66, Appl
                                              56349, A
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Pred. No. 1.2;
0; Mismatches 85; Indels 0
                                                    US-10-240 708-17

US-11-121-086-64

US-11-121-086-104

US-11-157-389-1

US-11-157-389-2

US-10-750-185-36299

US-10-750-185-36299

US-10-750-185-29912

US-10-750-185-29912

US-10-750-185-29912

US-10-750-185-29912
               US-10-750-185-31590
US-10-750-623-31590
US-10-750-185-56349
US-10-750-623-56349
                                                                                                                                                                                  US-10-750-623-37833
US-10-793-626-4227
US-10-392-234A-66
                                                                                                                                                      US-10-750-185-36704
US-10-750-623-36704
US-10-750-185-37833
                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.4
Matches 90; Conservative
                                   ) ORGANISM: Homo sapiens
US-11-121-086-107
4422222222
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NAME/KEY: exon
LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
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LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
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LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 216661..216952
JTHER INFORMATION: exon Qbis complement g34872 gene
      OTHER INFORMATION: 3'regulatory region g35018 gene
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
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NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
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LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872
FEATURE:
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OTHER INFORMATION: exon Q complement 934872
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U g35030 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S 935030 gene
                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 214676..214793
OTHER INFORMATION: exon T 935030 gene
                                                                             NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
FEATURE:
APPLICANT: Bougueleret, Lydie
APPLICANT: Bilahin Bernard
APPLICANT: Bilahin Bernard
APPLICANT: Bilahin Bernard
APPLICANT: Basioux, Laurent
FILE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE OF INVENTION SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
CURRENT APPLICATION NUMBER: US/11/145,703
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US/12/147,603
PRIOR PAPLICATION NUMBER: US 60/131,971
PRIOR PELING DATE: 1999-03-30
PRIOR PELING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR PELING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR PELING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR APPLICATION NUMBER: US 60/146,453
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PRIOR APPLICATION NUMBER: US 60/146,453

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LOCATION: 31.1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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OTHER INFORMATION: exon Bbis g35018 gene
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LOCATION: 65505..65853
OTHER INFORMATION: exon G g35018 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 65854..67854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E 935018 gene
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NAME:
NAME: exon
CONTINE: 1108..1289
OTHER INFORMATION: exon A g35018 gene
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LOCATION: 14877..14920
OTHER INFORMATION: exon B 935018 gene
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NAME/KEY: exon
LOCATION: 25593..25740
FEATURE: INFORMATION: exon C 935018 gene
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LOCATION: 29388..29502
OTHER INFORMATION: exon D 935018 gene
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LOCATION: 6466..64812
OTHER INFORMATION: exon F g35018 gene
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
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NAME/KEY:
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0; Gaps

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345257 Arriggreiraacaarriecraaacrirriargarecrarricaarcraaaccgreaaaa 345198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ACTIACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAATTT 140
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCAT
                                                                                                                                                                                                                                                                                                                                                                                             Length 1082144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59119, Application US/10750185
; Sequence 59119, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: PMI GENOMICS, INC.
; APPLICANT: ROLENEELD, David
; APPLICANT: ROLENEELD, David
; APPLICANT: ROLENEELD, David
; APPLICANT: PALTIN, Dennis
; TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; TILLE OF INVENTION: COMPOSITIONS
; FILLE REFERENCE: WALLIOG-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT APPLICATION NUMBER: US 60/437,482
; RILOR FILING DATE: 2002-12-31
; RILOR FILING DATE: 2002-12-31
; SEQ ID NOS: 64922
; SOFTWARE PATENTIN VERSION 3.1
; SEQ ID NO 59119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Score 32.6; DB 7; I
Pred. No. 1e+02;
0; Mismatches 79;
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                         FILE REFERENCE: ARCD:309US
CURRENT APPLICATION WUMBER: US/11/117,187
CURRENT APPLICATION WUMBER: US/09/531,120
PRIOR APPLICATION WUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SENGTH: 1082144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bovine 19866880452391
US-10-750-185-59119
                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.3%;
Matches 80; Conservative
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Best Local Similarity
Matches 59; Conserva
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Pred. No. 2.9;
0; Mismatches 72; Indels 0:
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OTHER INFORMATION: exon M1117 complement g34872 gene
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OTHER INFORMATION: exon M1090 complement 934872 gene
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OTHER INFORMATION: exon M1069 complement g34872 gene
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COCATION: 240528..240824
JTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
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MAME/KEY: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 240528..241685
OTHER INFORMATION: exon MI complement g34872 gene
                                                                                      WIHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                 NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
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LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872
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SOCATION: 240528..240617
                                                                  239719..239807
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
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LOCATION: 24053
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NAME/KEY: exon
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145 AGTIGITGACAATAICGACCGICTAAGITCCACACCGACGGCTATAAGAGITTCAITAIA 204 Gaps ö Length 1765; δ ద q

RESULT

; Sequence 211, Application US/11117187; Publication No. US20050266560A1; GENERAL INFORMATION:

RESULT 3 US-11-117-187-211/c

APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, GREGORY

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RESULT 8
US-10-240-708-73/c
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yequence 2918, Application US/1124368A
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yequence 2918, Application No. US20050287559A1
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yequence 2918, Application No. Sequence 2018
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Sequence 59119, Application US/10750623

Publication No. US2005028731A1

GENERAL INFORMATION:
APPLICANT: PMI GENOMICS, INC.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: RATIN, Dennis
ITLIE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOG-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US/10/750,623
FILE REPERENCE: MMILIOG-1
FRIENC PELLING DATE: 2002-12-31
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 59119
LENGTH: 1765
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57545, 57546, 5
57553, 57554, 5
57561, 57562, 5
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57575, 57576, 5
57583, 57584, 5
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NAME/KRY: misc_feature
NOCATION: 57531, 57532, 57533, 10CATION: 57540, 57541, 57542, 57543, 10CATION: 57540, 57549, 57550, 57551, 10CATION: 57556, 57557, 57559, 57559, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bovine 19866880452391
US-10-750-623-59119
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57573, 57574, 5
57581, 57582, 5
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LOCATION: 57564, 57565,
LOCATION: 57573, 57574,
LOCATION: 57581, 57582,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 59; Conserv
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US-11-124-368A-2918/c
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82012 AATAGAATGTATCAAACATTATAAATAGCAAATAATTATGTGTTGACTAAAAATACACAG 81953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 ATTAGCATCAATCTCCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGT 172
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Publication No. UG2005287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth

APPLICANT: Wouth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE REPERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT PILING DATE: 2005-05-26

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SECTION 1203
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Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dispense of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dispense of Diseases Associated with DNA Replication
FILE REPERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
CURRENT APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2238 TCAKCTCMARMRMCTCWCMMASTAMTWKTGSSAAAHWWMMAWWWRAMMTCATC 2292
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                                                                                                                                                               57602, 57603, 57604, 57611, 57612, 57613, 57619, 57620, 57621, 57629
LOCATION: 57589, 57590, 57591, 57592, 57593, 57594, 57595, 57596
OTHER INFORMATION: n = A,T,C or G
FEATURE:
                                                                                                                                                                                                                                                                                                                                                         Length 100000;
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                                                                                                                                                                                                                                                                                                                                                               y Match 11.6%; Score 31.8; DB 7; Length 1 Local Similarity 64.0%; Pred. No. 82; nee 48; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                  57601,
57610,
57618,
57626,
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rive 27; Mismatches
                                                                                                                                     NAWE/KEY: misc_feature

; LOCATION: 57897, 57898, 57599, 57600,

LOCATION: 57606, 57607, 57608, 57609,

; LOCATION: 57614, 57615, 57616, 57617,

LOCATION: 57622, 57623, 57624, 57625,

; CHER INFORMATION: n = A,T,C or G
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; ORGANISM: Rattus norvegicus
US-11-136-527-3203
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Matches 43; Conservative
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1007 rccaarirrirargrecrirarrriricrrarrirracaracacarcaacriatara 1066
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133 TCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGGTTCCACACCGACGGCTATAAG 192
                                                                                                                                                                                              US-10-750-623-39222

US-10-750-623-39222

Sequence 39222, Application US/10750623

GENERAL INFORMATION:
APPLICANT: MMI GENONICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: APPLICANT: ACENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
APPLICANT: PANTIN, Dennis
TITE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TILE OF INVENTION: METHODS AND SOUTH TRAITS
TILE OF INVENTION WIMBER: US/10/750,623
CURRENT FILING DATE: 2002-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 39222

LENGTH: 1140
TANDER OF ELENGTH: AVENIA
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; Sequence 37551, Application US/10750185
; Publication No. US2005026663A1
; CENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
ITLE OF INVERTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
ITLE REFERENCE: MAILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PELING DATE: 2002-12-31
NUMBER OP SEQ ID NOS: 64922
; SOFTWARE: PATENTIN Version 3.1
; SEQ ID NO 37551
LENGTH: 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.3%; Score 31; DB 6; Length 1140;
Best Local Similarity 52.8%; Pred. No. 32;
Matches 67; Conservative 0; Mismatches 60; Indels
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US-10-750-623-39222
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APPLICANT: MININGENOMICS, INC.
APPLICANT: MININGENOMICS, INC.
APPLICANT: MICHARA
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: APTES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-2
CURRENT FALICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PARENTIN VERSION 3.1
SEQ ID NO 39222
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 5152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.4%; Score 31.2; DB 6; Length 5
Best Local Similarity 45.8%; Pred. No. 46;
Matches 108; Conservative 0; Mismatches 128; Indels
           PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10013529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
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ORGANISM: Bovine 19866881347877
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-750-185-39222
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                                                                                                                                                                                                                                                                                         LENGTH:
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APPLICANT: Wyeth APPLICANT: Burc
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Sequence 6695, Application US/11136527
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION:
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086)
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: 108/023
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 37551
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Pred. No. 33;
0; Mismatches 75; Indels
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Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37551, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENTELD, David
; TYPE: DNA
; ORGANISM: Bovine 19866880663412
US-10-750-185-37551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bovine 19866880663412
US-10-750-623-37551
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milarity 50.3%; Conservative 0.
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ilarity 50.3%;
Conservative
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Best Local Similarity
Matches 76; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
FRIOR APPLICATION NUMBER: 0505-05-05
PRIOR APPLICATION NUMBER: US
PRIOR PILING DATE: 2005-05-26
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APPLICANT: Murcaynaki, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 CCTAAWWAWWWWWWWAAAARRWWAWAWWWTAGTTTCTTTTTACT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 CATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTCTTGACT
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CURRENT APPLICATION NUMBER: US/11/136,527
                    CURRENT FILING DATE: 2005-05-25
PRIOR PAPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 6695
LENGTH: 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2599, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 2599
LENCTH: 2217
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; ORGANISM: Rattus norvegicus
US-11-136-527-6695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Rattus norvegicus US-11-136-527-2599
                                                                                                                                                                                                                                                                                                                                               49; Conservative
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Best Local Similarity
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Matches 49; Conserv
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Best Local Similarity 47.2%; Pred. No. 64;
Matches 93; Conservative 0; Mismatches 104; Indels 0.
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Job time : 401 secs
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                                                                                                                                                                                                                                                              225 AGCAAATAATTTTTCT 241
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-206
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Sequence 1, Appli
Sequence 83537, A
Sequence 14150, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 15866, A
Sequence 12866, A
Sequence 12201, A
Sequence 12201, A
Sequence 13201, A
Sequence 13201, A
Sequence 13201, A
Sequence 13365, A
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Sequence 12201, A
Sequence 13365, A
Sequence 112718,
Sequence 112802,
Sequence 112962,
Sequence 112962,
                                                                                                   ; Search time 148 Seconds (without alignments) 3290.891 Million cell updates/sec
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2: /cgn2 6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6_COMB.seq:*
4: /cgn2 6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2 6/ptodata/1/ina/PCOMB.seq:*
7: /cgn2 6/ptodata/1/ina/PCOMB.seq:*
8: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PB_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/RB_COMB.seq:*
GenCore version 5.1.6
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US-09-733-685-1

US-09-949-016-83537

US-09-949-016-14150

US-09-813-356-1

US-09-813-356-3

US-09-813-356-3

US-09-813-356-3

US-09-813-356-3

US-09-813-356-1

US-09-949-016-1666

US-09-949-016-11201

US-09-949-016-112062

US-09-949-016-112062

US-09-949-016-112062

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US-09-949-016-112062

US-09-949-016-114858

US-09-949-016-14858

US-09-949-016-14858

US-09-949-016-14858

US-09-949-016-14858

US-09-949-016-14858

US-09-949-016-14858
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
, Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                       January 12, 2006, 00:16:10
                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                            US-10-800-161-28
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Match Length DB
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13.8 319608
13.6 1963
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13.6 1963
12.6 227390
12.6 227390
12.5 227390
12.5 601
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12.5 601
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Perfect score:
                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                  Seguence:
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Sequence 2, Appli Sequence 1803, A Sequence 2708, Ap Sequence 263, Appl Sequence 15274, A Sequence 15274, A Sequence 13703, A Sequence 13703, A Sequence 29, Appl Sequence 29, Appl Sequence 1274, Ap Sequence 1274, Ap Sequence 11782, A Sequence 11783, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 11784, A Sequence 19931, A Sequence 19031, A	IN THE REGULATION OF	element
US-08-526-840B-2 US-09-621-976-18033 US-09-949-016-2708 US-09-949-016-263 US-09-949-016-15274 US-09-949-016-15274 US-09-949-016-15274 US-09-949-016-15274 US-09-949-016-13703 US-08-526-023-29 US-08-526-023-29 US-09-596-002-36 US-09-596-002-36 US-09-949-016-17030 US-09-949-016-11782 US-09-949-016-11782 US-09-949-016-11782 US-09-949-016-11782 US-09-949-016-11783	ALIGNMENTS US/09733685 cca M Robert A ENDER ENCODING PROTEINS INVOLVED HAR GENE EXPRESSION IN PLANTS 189A MERR: US/09/733,685 2000-12-08 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-12-15 199-13-199	motif motif R22 element AS1 salicylic acid response AX2 GAN GAN GENOMIC CODING region
34 12.4 2275 3 33.6 12.3 474 3 33.6 12.3 3244 3 33.6 12.3 3953 3 33.6 12.3 12797 3 33.4 12.2 2735 3 33.4 12.2 67755 3 33.2 12.1 666 2 33.2 12.1 139949 3 33.2 12.1 139949 3 33.2 12.1 139949 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3 33.2 12.1 139952 3	85-3 3, Application 5, 6706952 NFORMATION: T: Cade, Rebe TT: Dietrich, VINVENTION: SERENCE: A-310 APPLICATION NUME FILING DATE: 15 PELING DATE: 15 PELING DATE: 15 PELING DATE: 15 PELING DATE: 15 PELING DATE: 15 PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME PELING DATE: 15 PERIOR NUME	maisc_feature (365)(374) misc_feature (426)(435) MEMATION: TCA1 misc_feature (609)(614) misc_feature (605)(614) misc_feature (646)(665) MEMATION: CAWV misc_feature (707)(712) Misc_feature (707)(712) Misc_feature (707)(712) Misc_feature (707)(712) Misc_feature (757)(762) Misc_feature (757)(762)
000000000 0000 0 000000000000000000000	RESULT 1 US-09-733-685- SEQUENCE 3, PATENT NO. 6 GRENERAL INFO APPLICANT: TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN FILE REPERF CURRENT FILE CURRENT FILE PRIOR FILLI PR	INAME/KEY: LOCATION: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO: NAME/KEY: COTHER INFO:

99.4%; Score 272.4; DB 3; Length 1700;

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; Fatent No. 670692
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
; APPLICANT: Dietrich, Robert A
; TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
; TITLE OF INVENTION: SAR GENE EXPRESSION IN PLANTS
; TITLE OF INVENTION: SAR GENE EXPRESSION IN PLANTS
; CURRENT PILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/175,519
; PRIOR APPLICATION NUMBER: 60/175,519
; PRIOR APPLICATION NUMBER: 60/175,519
; PRIOR APPLICATION NUMBER: 60/175,519
; PRIOR APPLICATION NUMBER: 60/175,519
; ROFWARE: Patentin Ver. 2.1
; SEQ ID NO:
LIBRGATE: 509
                                                                                                                                                                                                                                                                     240
                                                                        578 TCTAAAAATATAGCGGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA 637
                                                                                                                           ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                            697
                                                                                                                                                                                                CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                                                 757
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                                                                                                                                           1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                Gaps
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                1; Indels
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Pred. No. 1.2e-05;
0; Mismatches 2;
Pred. No. 5.8e-68;
                                                                                                                                                                                                                                                                                                                                                                             rrgacraagcrraaacgacgcccrraacarrrrc 851
                0; Mismatches
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CCATION: (68)..(433)

CTHER INFORMATION: gene product NI16

NAME/KEY: misc feature

CCATION: (1447)..(147)

CTHER INFORMATION: Sall site

NAME/KEY: misc feature

CATHER INFORMATION: Sall site

CCATION: (344)..(349)

US-09-733-685-1
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ORGANISM: Arabidopsis thaliana
Best Local Similarity 99.6%;
Matches 273; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.4%;
Matches 54; Conservative
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Sequence 83537, Application US/09949016 Patent No. 6812339 PRERAL INFORMATION: APPLICANT: VENTER, J. Craig et al.

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US-09-949-016-14150

Sequence 14150, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PLING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 14150

LENGTH: 49440
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBENCE: CL00130.
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR PEDILORION NUMBER: 66/241,755
PRIOR PEDILORION NUMBER: 66/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 66/237,768
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 83337
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 IGACGICATGATACTTACGCTTTAAAACATCGCATGATGATGATGATTAGCATCAATTTCC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.2%; Score 39; DB 3; Length 601; 51.4%; Pred. No. 0.11; ive 0; Mismatches 85; Indels
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Best Local Similarity 51.4
Matches 90; Conservative
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Best Local Similarity 51.4
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-83537
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US-09-949-016-14150
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CCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
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LOCATION: 216661..216952
JTHER INFORMATION: exon Qbis complement 934872 gene
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JTHER INFORMATION: exon Obis complement g34872 gene
                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
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LOCATION: 229647..229742
DIHER INFORMATION: exon X complement g34872 gene
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NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
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OTHER INFORMATION: exon P complement 934872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U 935030 gene
                                                                                        NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon G g35018 gene
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NAMES EXON
LOCATION: 201188. 201234
OTHER INFORMATION: exon S 935030 gene
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LOCATION: 214676..214793
OTHER INFORMATION: exon T 935030 gene
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NAME/KEX: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
                                        OTHER INFORMATION: exon F 935018 gene
                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
                  64666..64812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                       GENERAL INCRAMICANT:

APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bilain, Bernard
APPLICANT: Bilain, Bernard
APPLICANT: Bilain, Bernard
APPLICANT: Bilain, Bernard
APPLICANT: Bilain, Bernard
APPLICANT: Bilain, Bernard
APPLICANT: Blumenfeld, Laurent
TILLE REPERENCE: GENEST: 044005
CURRENT FILING DATE: 2000-03-30
PRIOR PELICATION NUMBER: US 60/126,903
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR PELICATION NUMBER: US 60/131,971
PRIOR PELICATION NUMBER: US 60/145,928
PRIOR FILING DATE: 1999-07-14
PRIOR PELICATION NUMBER: US 60/145,915
PRIOR PELICATION NUMBER: US 60/145,928
PRIOR PELICATION NUMBER: US 60/146,453
PRIOR PELICATION NUMBER: US 60/146,453
PRIOR PELICATION NUMBER: US 60/146,452
PRIOR PELICATION NUMBER: US 60/146,453
PRIOR PELICATION NUMBER: US 60/16,288
PRIOR PELICATION NUMBER: US 60/16,384
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
                          LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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OTHER INFORMATION: exon Bbis 935018 gene
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NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C g35018 gene
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NAME/KEX: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E g35018 gene
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NAME/KEY: exon
LOCATION: 14877..14920
OTHER INFORMATION: exon B g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon D g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 1108..1289
OTHER INFORMATION: exon A g35018 gene
                                                                                                                           RESULT 5
US-09-539-333D-1
Sequence 1, Application US/09539333D
Patent No. 6476208
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 29388..29502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 31..1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 319608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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57915 AAAGGAGAAAAATGAGGCACCACCCTCTTTA 57947
                  158 ATCGACCGTCTAAGTTCCACACGGCTATA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 199122..201122
OTHER INFORMATION: 5'regulatory region
LOCATION: 201123..201234
OTHER INFORMATION: exon S
NAME/KEY: exon
LOCATION: 201123..201560
OTHER INFORMATION: exon S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: 217671..217764
OTHER INFORMATION: exon VI
NAME/KEY: exon
LOCATION: 227655..227736
OTHER INFORMATION: exon V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 214676..214793
OTHER INFORMATION: exon T
NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U
NAME/KEY: exon
LOCATION: 216836..216994
OTHER INFORMATION: exon V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 216836..217077
OTHER INFORMATION: exon V2
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 240440..241153
OTHER INFORMATION: exon W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 238715..238919
THER INFORMATION: exon V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 240440..240673
OTHER INFORMATION: exon W
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 241072..241291
OTHER INFORMATION: exon X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
                                                                                                                             US-09-679-409-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 GACTICCITIATICCAAAAGICAATAAAGIGIGACGICAIGAIACITAACGCITIAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.8%; Score 37.8; DB 3; Length 319608; Best Local Similarity 52.9%; Pred. No. 1.1; Matches 81; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                               |AME/KEY: exon
ACCATION: 240528..240569
NTHER INFORMATION: exon M1117 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                         KEY: exon
ION: 240528..240596
INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEY: exon
ION: 240528..240617
INFORMATION: exon M1069 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
                                                                                                                         NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g14872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: exon
LOCATION: 240528..240644
DTHER INFORMATION: exon MS2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
LOCATION: 231870..231879
OTHER INFORMATION: exon Ol complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCATION: 240528..241685
THER INFORMATION: exon M1 complement g34872 gene
                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
                                                   NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
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NAME/KEY: exon
LOCATION: 292653..292841
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FION:
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: variable motif AAAGG or GAAGGAAGGAAGGAAGA 57795 GAACTIGIATCTICCCACIGIGICIACAIGGIGACTICCTAATTICACCCATATATACAG 57854 GACTICCITIALICCAAAAGICAALAAAGIGIGACGICAIGAIACTIACGCITIAAAACA 97 0; Gaps Score 37.8; DB 3; Length 319608; Pred. No. 1.1; 0; Mismatches 72; Indels 0: NAME/KEY: allele

LOCATION: 210864

OCHER INFORMATION: 8-282-260 : polymorphic base G or T
NAME/KEY: allele

LOCATION: 210979

OCHER INFORMATION: 8-282-245 : polymorphic base A or C
NAME/KEY: allele

LOCATION: 21050

OCHER INFORMATION: 8-282-174 : variable motif AAAGG or GAA

NAME/KEY: allele

LOCATION: 211050

OCHER INFORMATION: 8-282-174 : variable motif AAAGG or GAA

NAME/KEY: allele

LOCATION: 21132

OCHER INFORMATION: 8-282-92 : polymorphic base A or T

NAME/KEY: allele

LOCATION: 21137

OCHER INFORMATION: 8-281-367 : polymorphic base A or G

OCHER INFORMATION: 8-281-367 : polymorphic base A or G NAME/KEX: allele LOCATION: 207313 OTHER INFORMATION: 8-251-322 : polymorphic base A or G NAME/KEY: allele LOCATION: 208285 OTHER INFORMATION: 8-289-322 : polymorphic base A or G NAME/KEY: allele LOCATION: 208960 OTHER INFORMATION: 8-287-249 : polymorphic base C or T NAME/KEY: allele LOCATION: 209123 OTHER INFORMATION: 8-287-86 : polymorphic base A or T : polymorphic base G or C : polymorphic base C or T ტ U : polymorphic base A or C Ü : polymorphic base G or C : polymorphic base A or G : polymorphic base A or : polymorphic base A or : polymorphic base G or : polymorphic base A or G or OTHER INFORMATION: 8-293-130 : polymorphic base A or : polymorphic base C or : polymorphic base NAME/KEY: allele
OCCATION: 210361
OCTHER INPORMATION: 8-283-278:
NAME/KEY: allele
LOCATION: 210463
OCTHER INPORMATION: 8-283-176:
NAME/KEY: allele
LOCATION: 210486
OCTHER INPORMATION: 8-283-153:
NAME/KEY: allele
LOCATION: 210583
OCHER: INFORMATION: 8-283-56:
NAME/KEY: allele
LOCATION: 210583
OCHER: INFORMATION: 8-283-56:
NAME/KEY: allele
LOCATION: 210879
OCHER: INFORMATION: 8-283-56:
OCHER: INFORMATION: 8-283-56: Query Match 13.8%; Best Local Similarity 52.9%; Matches 49.81; Conservative (8-279-197 NAME/KEY: allele LOCATION: 212821 OTHER INFORMATION: 8-278-289 NAME/KEY: allele OTHER INFORMATION: 8-281-299 LOCATION: 211366 OTHER INFORMATION: 8-281-248 8-285-319 8-292-198 NAME/KEY: allele LOCATION: 212520 OTHER INFORMATION: NAME/KEY: allele LOCATION: 209631 OTHER INFORMATION: NAME/KEY: allele LOCATION: 206545 OTHER INFORMATION: NAME/KEY: allele LOCATION: 211315 NAME/KEY: allele LOCATION: 211366 38 98

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Sequence 3, Application US/09813356 Patent No. 6730826
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.8%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.8%;
Matches 108; Conservative
                                                                                   TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: exon
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                                                                                                                                                                     | LOCATION (1853) .. (1963) | NAME/KEY: CAAT signal | LOCATION (1669) .. (1672) | NAME/KEY: TATA signal | LOCATION (1775) .. (1778) | NAME/KEY: GC signal | LOCATION (1806) .. (1807) | NAME/KEY: promoter | LOCATION (1) .. (1852) | US-09-813-356-1
                                             SEQ ID NO 1
LENGTH: 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-813-356-3
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  57855 TTGCTTGTGAATGTCTTTATCTTCAATGTCAGCCGTCCAAAAGAGTAAAAAGAGAAAAAC 57914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850 TATAAATTTACGAGTTTACTATACTTTAGTCGTACAGTTTGCAATAATAGTATTTAACC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGACGTC 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 TICATTATAAATTITAGCAAAATAAAATCAGCAAATAATTITTTCT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: George, Wagner
APPLICANT: Susheng, Gan
APPLICANT: Erming, Wang
APPLICANT: Rui, Wang
APPLICANT: Rui, Wang
TITLE OF INVENTION: Trichome Specific Regulatory Sequence
FILE REFERENCE: 50229-260
                                                                                                                                                                                     Sequence 2, Application US/09813356
Patent No. 6730826
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: George, Wagner
APPLICANT: Erming, Wang
APPLICANT: Rui, Wang
APPLICANT: Rui, Wang
TITLE OF INVENTION: Trichome Specific Regulatory Sequence
PILE REFERENCE: 50229-260
                                                                                   57915 AAAGGGAGAAAAAAAGAGGCACCACCTCTTTA 57947
                                             158 ATCGACCGTCTAAGTTCCACACCGACGGCTATA 190
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/813,356
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,088
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2001-03-21
PRICR APPLICATION NUMBER: US 60/191,088
PRIOR FILING DATE: 2000-03-22
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, Sequence 1, Application US/09813356
, Patent No. 6730826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CAAT signal
| LOCATION: (1669)..(1672)
| NAME/KEY: GC_signal
| LOCATION: (1806)..(1807)
| US-09-813-356-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: promoter
LOCATION: (1)..(1852)
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                                                                                                                     16 GATACCAATTTTTCCACACGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGACGTC
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      Length 1963;
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APPLICANT: George, Wagner

APPLICANT: Susheng, Gan

APPLICANT: Statemer

APPLICANT: Statemer

APPLICANT: Rui, Wang

TITLE OF INVENTION: Trichome Specific Regulatory Sequence

FILE REFERENCE: 50229-260

CURRENT APPLICATION NUMBER: US/09/813,356

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,088

PRIOR PILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.2; DB 3; Length 1 Pred. No. 0.47; 0; Mismatches 118; Indels
Score 37.2; DB 3; Length 1 Pred. No. 0.47; 0; Mismatches 118; Indels
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0; Gaps

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, LOCATION: (1)..(1141)

; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
                                                                                                                                                                                                                                                                                                         166 TCTAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCA 225
                                                                                                                                                                                566 WYWSNNAMWYRRYSARNWSSMARWITRNNWWNSGBVRWRWAGTWWWRHWNNNTDTRYYW 507
                                                                                                                                                   46 TIATICCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGA 105
                                                                                                                                                                                                                                                                                                                                                                                                                 506 WWKRWARBTTTYYDSMCNAKSMWRGINWRAMKMWWAANNDAGAMDHWTY 458
                                                                                                                                                                                                                                                                                                                                                                                         226 GCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                     Query Match
12.6%; Score 34.6; DB 3; Length 1141;
Best Local Similarity 11.4%; Pred. No. 2.2;
Matches 26; Conservative 97; Mismatches 106; Indels 0
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US-09-949-016-13365/c
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US-09-949-016-15866/c
; Sequence 15866, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    ATILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WHEN US/09/949,016
; TITLE OF INVENTION: WHENER US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: PSELSEQ for Windows Version 4.0
; SEQ ID NO 15866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10562 AACTCTCCTCTGGCTTAGTTAGCTTCACACTATATTCCTTGTCTGAATTCCTCGACTT 10503
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  790 ITAGATAATAGTTACTACTATTTGTCATGAAAATATCAATAGATACAAATTTAAAGTGAC 849
                                           AATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGT 195
                                                                             850 TATAAATTTACGAGTTTACTATACTTTAGTCGTACAGTTTGCAATAATAGTATTTTAACC 909
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Patent No. 6784342

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03

PRIOR PILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.0

SEQ ID NO 22
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                                                                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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ORGANISM: Artificial sequence
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Best Local Similarity 54.1%;
Matches 72; Conservative
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NAME/KEY: promoter
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US-09-949-016-15866
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161269 Tricacgaalaalaalaalarateriegraficarracrafracriteccararrecritarer 161210
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OTHER INFORMATION: n = A,T,C or G
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Query Match
12.5
Best Local Similarity 48.2
Matches 96; Conservative
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ORGANISM: Human
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US-09-949-016-112718/C
i Sequence 112718, Application US/09949016
j Patent No. 6812339
j GENERAL INFORMATION:
j APPLICANT: UNIVERAL OF INVENTION:
j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
j TITLE OF INVENTION WIMBER: US/09/949,016
j CURRENT APPLICATION NUMBER: 00/241,755
j PRIOR APPLICATION NUMBER: 60/241,755
j PRIOR FILING DATE: 2000-10-20
j PRIOR FILING DATE: 2000-10-03
j PRIOR FILING DATE: 2000-10-03
j PRIOR FILING DATE: 2000-09-08
j NUMBER OF SEQ ID NOS: 207012
j SOFTWARE: FastSEQ for Windows Version 4.0
j SEQ ID NO 112718
              GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 13365

LENGTH: 227391
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Pred. No. 2.5;
0; Mismatches 103;
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Sequence 13365, Application US/09949016
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US-09-949-016-13365
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Best Local Similarity 48.2%;
Matches 96; Conservative
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LOCATION: (1)...(22739:
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US-09-949-016-112718
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ORGANISM: Human
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| Sequence 1128012, Application US/09949016
| Sequence 1128012, Application US/09949016
| Patent No. 681233
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TILLE OF INVENTION: 000-04-14, 755
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-0-0-08
| WUMBER OF SEQ ID NOS: 207012
| SOFTWARE: PastSEO for Windows Version 4.0
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                                                                210 AGGCAACCACAGTTTTGCTTTTTCTGATATTTTTATTAAAAGGAATTATAAAATAGGTA 151
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12 AGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGA 71
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48.2%; Pred. No. 2.5;
tive 0; Mismatches 103; Indels
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source
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BZ770600 SALK 1435
BH814587 SALK 0666
BZ352865 SALK 0827
BZ019485 oeg72g05.
BE063458 BP66458
BS2379 CIT-HSP-200
A1990512 wa40e09.x
R88734 yp93b07.s1
AL106628 DE060phil
AL106628 DE060phil
AL1290306 GM02a04.x
A1290306 GM02a04.x
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A1620654 tu85c06.x
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AI151151 qc87f07.x
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                                                                    January 12, 2006, 00:02:06; Search time 3802 Seconds (without alignments) 3371.820 Million cell updates/sec
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BU689059 0
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                          residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/ organism="Arabidopsis thaliana"
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/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
This is single pass sequence lies within 300 bases of the 5' end of
At3g25882.
Class: TDNA tagged.
Location/Qualifiers

23	42	15.3				995524	BM9	BM995524	UI-H-DT1-
42	42	15.3				BQ015514	BQ01	5514	UI-H-EIl-
25	42	15.3	684			003373	900E	3373	-EI
26	42	15.3				006479	BQ00647	6479	
27	42	15.3				447735	CA44	7735	-013-H-IO
	42	15.3	2026			AF116653	AF11	AF116653	Homo sapı
53	1.6	15.2				423473	BP4	24.0	BF4234/3
	41.6	15.2				494002	AI4S	2004	qz9/10/.X
	41.6	15.2				708769	AL/C	7070	hv61010 ×
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	1.4	15.1				051787	AWO	18/10	WZU3CII.X
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	41.4	15.1				501745	BES(BE501745	hw34f10.x
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	σ	14	47	~		AA936680	AA93	99	ol79b04.8
45 3	8.	14.5	52	8		435057	A143	35057	th82c12.x
						ALIGNMENTS			
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LOCUS	BZ352867	2867				228 bp DNA	linear	SSS	
DEFINITION	SALK	0827 Idope	24.45.	05.x	Ar	SALK 082724.45.05.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 082724.45.05.x,	na TDNA insel K 082724.45.(rtion J5.x,	lines genomic
	Bury	ey se	survey sequence)		I		
ACCESSION	BZ35	BZ352867							
VERSION	BZ35	BZ352867.1		GI:24943729	372				
KEYWORDS	GSS.		٠						
SOURCE	Arab	idopi	Arabidopsis thaliana	lian		(thale cress)			
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	Buka	ryota	i; Viri	dıb	ant	Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Ifacheophyta	i; Empryopnyto	, ,	circopiiy ca;
	Sper	mator	hyta;	Magn	ilo.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty.	Ledons; core	eudi	Ledons
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AUTHORS	Alon	Bo, J.	A., Le	1886	Ë,	Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, K.	Chen, H., Chel	Cneuk, K.	, Dradnie I.
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	Salk	Inst	itute	Genc	mic	Salk Institute Genomic Analysis Laboratory	tory (SIGnAL)	_	
	The	Salk	Instit	ute	for	Biological Stud	lies		
	100	2	Torrev	ā	8	Road, La Jolla,	CA 92037, USA	4	
	1 6	Tel . 858	453 4100 x1752	0	175				
		200	55 B 53	, 62					
	Email	1: 6	ecker@salk.edu	1k.e	ggn				

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вны14587 2002 237 bp DNA linear GSS 02-MAY-2002 SALK 066674 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 066674, genomic survey sequence. BH814587
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                   61 cGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
Fax: 858 558 6379
                      Indels
al Similarity 100.0%; Pred. No. 2.9e-28; 152; Conservative 0; Mismatches 0;
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Addrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
1181: 858 453 4100 x1752
Pax: 858 558 6379
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                                                                         Score 222; DB 9; Length 228;
Pred. No. 4.3e-46;
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/ecotype="Col-0"
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BP863458
                  KEYWORDS
SOURCE
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                                                                                                                                           AUTHORS
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 VERSION
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                                                                     B2352865 14-NOV-2002 SALK 082722.32.45.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_082722.32.45.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Arabidopsis thaliana TDNA insertion lines"
hote="PCTK was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alon80,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCGTCTAAGTTCCACACCCGACGCTATAAGAGTTTTCATTATAAATTTTAGCAAAATAAAA 221
                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3925882.
Class: TDNA tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="SALK_082722.32.45.x"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ATCAGCAAATAATTTTTTTTTTGACTAAGCT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAGCAAATAATTTTTTTTTGACTAAGCT 251
                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
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/ecotype="Col-0"
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                                                                                                                                                                 BZ352865.1 GI:24943727
                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                               VERSION
KEYWORDS
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BP863458 RAFL21 Arabidopsis thallana cDNA clone RAFL21-66-M11 5', mRNA sequence.
BP863458
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="boleracea02"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Obborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
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Brassica oleracea
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II, Brassicales, Brassicaceae, Brassica.
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Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Seki M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K.,
Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA-ATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAAT
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8
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                                                                                                                        1 (bases 1 to 691)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R.
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639 recharadaagagraneerearaaraaaccaaaaraaar 678
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wateon.wustl.edu
Plate: oeg72 row: g column: 05
Seq primer: -28RPpOT reverse
Class: shotgun
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High quality sequence stop: 551.
Location/Qualifiers
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organism="Homo sapiens"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                  85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                               Contact: Motoaki Seki
Plant Functional Genomics Research Group
Plant Functional Genomics Research Group
RIKEN Genomic Soziences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-4359
Email: mseki@rtc.riken.go.jp
An Arabidopais full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998, 2002). This clone is in a modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and http://rarge.gsc.riken.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIT-HSP-2003E3.TF CIT-HSP Homo sapiens genomic clone 2003E3, genomic survey sequence.
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mtMA"
/db xref="taxon:3702"
/db xref="taxon:3702"
/clone="RAFL21-66-M11"
/lab host="BH10B"
/clone lib="RAFL21"
/note="Site 1: BamH1; Site 2: Sal1; Subtraction Library.
The sequence was obtained from samples subjected to various stress and plant hormones-treated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21
Class: BAC ends.
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1 (bases 1 to 465)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  , Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and
                                     Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 GCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCAAATAATTTTTTTCTTGACTAAGCTTAAACGACGCCGTTAACATTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.9%; Score 49; DB 3; Length 397; Best Local Similarity 100.0%; Pred. No. 0.056; Matches 49; Conservative 0; Mismatches 0; Indels

    .397
    /organism="Arabidopsis thaliana"

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1. .465
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B52379/c
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source

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Donaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGBA clone distribution information can be

Clone distribution: NCI-CGBA clone distribution information can be

Cound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 444.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP_GC4 was prepared, and
se circles were made in vitro. Following HAP purification,
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w840e09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2499688 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 TAATGAAGTAGGAGGCAAGATTATCCATTGAAGGTATTATTATATGCAGCTCATCTTAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 CCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 grgacaaarrccaracagaagacraraacagaaarcacararrraararraaaarraar 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 609)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-r@mail.nih.gov
Itisgue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 TGATGATGTCATTAGCATCACCACCGTCCAATTTATTTAGTTGTTGACAATATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                            /sex="Male"
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII
                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 45.4; DB 9; Length 4
56.3%; Pred. No. 0.47;
ive 0; Mismatches 66; Indels
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/mol_type="mRNA"
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/clone="IMAGE:2499688"
/issue_type="pooled germ cell tumors"
/lab_hoge="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 ACTTCAAATATCTTTCACATTAAGATGATTA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 TCAGCAAATAATTTTTTTTGACTAAGCTTA 253
/mol_type="genomic_DNA"
/db_xref="GDB:7038437"
/db_xref="taxon:9606"
/clone="2003E3"
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AI990512.1 GI:5837393
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this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 692
High quality sequence stops: 260
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the Insert Length: 692 Std Brror: 0.00
Seq primer: Promega -21m13
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/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen, Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site I: Pac I; Site 2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R88734 321 bp mRNA linear EST 24-AUG-1995
yp93b07.81 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:194965 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                              124 TCTCCACCGTCCAATTTATTTAGTTGACAATATCGACCGTCTAAGTTCCACACCGAC 183
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                  3 rrrccarrigaegrarrarrrarrrigcaecrcarcrraagreacaaaarrccaracaeaa 62
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 321)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                          ö
                                                                                                                                                                        DB 1; Length 609;
                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                           Score 43.6; Di
Pred. No. 1.4;
0; Mismatches
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Location/Qualifiers
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/db_xref="GDB:3764015"
/db_xref="taxon:9606"
/clone="IMAGB:194965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                        Query Match
Best Local Similarity 58.5%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R88734.1 GI:953561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ACTAAGCTTA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AAGATGATTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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VERSION
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JOURNAL
COMMENT
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                                                                                                                             ORIGIN
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etudé du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AIACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAAT 138
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                                                                                                                                                                                                                                                                                                                                               63
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit
                    double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                              180 CGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTT
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                                                                                                                                                                                                                                                                                                 120 TCAATCTCCACGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTT 3'],
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                                                                                                                                                                                              Query Match 15.7%; Score 43; DB 8; Length 321; Best Local Similarity 56.7%; Pred. No. 1.9; Matches 76; Conservative 0; Mismatches 58; Indels
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Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila mel
/mol type="genomic DNA"
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/clone="lb="DrosBAC"
/plasmid="pBelobaC11"
/note="end:77"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACNIŠA12 of DroeBAC library fi
fly), genomic survey sequence.
AL106628
AL106628.1 GI:5622852
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DEFINITION
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VERSION
KEYWORDS
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/do_xerfe="txxxon:9606"
/clone="InAGE:2362153"
/lab_host="DH10B"
/clone="Drgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.R. Clones 297480-302087; 682632-687239, 726408-728711, and 729096-7313199. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                     289 bp mRNA linear EST 19-DEC-1999 wf85111.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2362125 3', mRNA Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS A1290306 360 bp mRNA linear EST 29-JAN-1999
DEFINITION qm02a04.x1 Soares_NhHMPu_S1 Homo sapiens CDNA clone IMAGE:1880622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (base 1 to 289)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 498 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TITCCATTGAAGGTATTATTTATTTGCAGCTCATCTTAAGTGACAAAATTCCATACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                            AI873432.1 GI:5547481
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     244 ACTAAGCTTA 253
                                                    123 AAGATGATTA 132
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Best Local Similarity
Matches 75; Conserv
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AI873432
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Life Technologies catalogg #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 957 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIS40689 115 bp mRNA linear EST 14-APR-1999 tn72all.xl NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2175068 3' similar to contains element THR repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                 1010 HEMMAHAMMAMMAMTHAHATHHWITHMINAMHAHITMAHAHIMINAMAMAMAMIHITITMAHHH 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="NCI_CGAP_Lyml2"
//note="Organ: lymph node; Vector: pCMV.SPORT6; Site_1:
//note="Organ: lymph node; Vector: pCMV.SPORT6; Site_1:
Sall; Site_2: Not!, Cloned unidirectionally. Primer:
Oligo dT. Areage insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
890 MANITTHITHITHITHINAMINAMINAMINITHINITHINITHINAMINAMITTHITHITTI 949
                                                                                139 TTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTC 198
                                                                                                                                                                                         199 ATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTCTTGACTAAGCTTAAAACGA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACAGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 GCCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTCTTG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TATCCATTGAAGGTATTATTTTTGCAGCTCATCTTAAGTGACAAAATTCCATACAGAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (Dases 1 to 135)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapberremail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DH10B"
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                                                                                                                                                                                                                                                                                                  259 CGCCGTTAACATTTT 273
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hes 75; Conserv
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AUTHORS
TITLE
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AI540689
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244 ACTAAGCTTA 253
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AI261719
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AI261719
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/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/clone with a maddfied polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA-from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH9M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GACTATAACAGAAATCATATTAATATTAAAATTAATACTTCAAATATCTTTCACATT 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1880622"
/tisuse type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                       1 (Dasses to 360)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 833 Scd Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AI620654.1 GI:4629780
                                    AI290306.1 GI:3933080
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mRNA sequence.
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Best Local Similarity
                                                                                                      sapiens
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VERSION
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                                                          KEYWORDS
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP Clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/Amage/Amage.html
Insert Length: 486 Std Brror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 415
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/clone_lib="NCI_CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sal1;
/inote="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sal1;
/laberage linear: Oloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1 (bases 1 to 418)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:2257834"
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Unpublished (1997)
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Emmert Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Libri at:

Www-bio.llni.gov/bbrp/image.html

Insert Length: 400F from Gibco

Seq primer: 400F from Gibco

High quality sequence stops: 416.
fissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                          1. .421
/organism="Homo sapiens"
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/clone="twAGE:2028457"
/lab_host="DH108"
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0; Gaps Query Match 15.3%; Score 42; DB 1; Length 421; Best Local Similarity 57.7%; Pred. No. 3.4; Matches 75; Conservative 0; Mismatches 55; Indels

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244 ACTAAGCTTA 253

123 AAGATGATTA 132

Search completed: January 12, 2006, 02:15:10 Job time : 3811 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                     January 11, 2006, 22:55:15; Search
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ALIGNMENTS

NI16; transgenic; herbicide resistance; mouse-ear cress; promoter; ds. Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of Arabidopsis thaliana NI16 promoter DNA #5. SYGN) SYNGENTA PARTICIPATIONS AG Cade RM, Dietrich RA, Lawton KA; ADR16847 standard; DNA; 274 BP 15-DEC-1999; 99US-0171008P. 11-JAN-2000; 2000US-0175519P. 08-DEC-2000; 2000US-00733685. 20-JAN-2004; 2004US-00760752. 12-MAR-2004; 2004US-00800161 (first entry) Arabidopsis thaliana WPI; 2004-580223/56. US2004154051-A1. 21-0CT-2004 05-AUG-2004 interest ADR16847

The present invention relates to an Arabidopsis NII6 gene promoter useful in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica, pseudomonas syringae, Cercospora nicotianse, Peronospora parasitica. The

Claim 1; SEQ ID NO 28; 39pp; English.

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is used in the exemplification of the invention.
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present sequence is Arabidopsis thaliana NI16 promoter DNA. This sequence
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                                                                                           Gaps
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                                                                 Length 274;
                                                                                                                     TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTAT
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                                       Sequence 274 BP; 91 A; 58 C; 36 G; 89 T; 0 U; 0 Other;
                                                                Score 274; DB 13;
Pred. No. 5.2e-64;
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                in the exemplification of the invention.
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                                                                                          0; Mismatches
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11-JAN-2000; 2000US-0175519P.
08-DEC-0004; 2004US-00760752.
20-JAN-2004; 2004US-00760752.
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                                                                            Similarity
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                                                                                                                                                                                                                                                                                                       121 CAATCTCCACCGTCCAATTTATTTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                     TCTAAAAATATAGCCGATACCAATTTTTCCACACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                             GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI16; transgenic; herbicide resistance; mouse-ear cress; promoter; ds
                                                                                                                                                                                                                                                                  CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                                                          ;
0
                                       DB 13; Length 274;
                                                                          Indels
                                                                                                                 1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTT
Sequence 274 BP; 92 A; 58 C; 35 G; 89 T; 0 U; 0 Other;
                                     Score 272.4; DB 13
Pred. No. 1.4e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                        rrdacraagcrraaacgacgccgrraacarrrrc 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana NI16 promoter DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; SEQ ID NO 27; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2004; 2004US-00800161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0171008P.
                                       99.4%;
                                                      ilarity 99.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR16846 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietrich RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-580223/56.
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004154051-A1.
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Sequence 862 BP; 337 A; 112 C; 152 G; 261 T; 0 U; 0 Other;
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11-JAN-2000; 2000US-0175519P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004248303-A1
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                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2005
                                                                                                                                                                                                                                                                                                                                              ADV66225;
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                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
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                                                                                                 271 rcraaaaararagccgaraccaarrrrrccacacarggacrrccrraraccaaagrca 330
                                                                                                                       AIAAAGIGIGACGICAIGAIACITAACGCITIAAAACAICGCAIGAIGAIGACGITAGCAI 120
                                                                                                                                             331 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 390
                                                                                                                                                                    CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                               GACGCCTATAAGAGTTTCATTATAAATTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
                                                                                                                                                                                                                                    510
                                                                                                                                                                                        CAATCTCCACCTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 450
                                                                              9
                                                                                                                                                                                                                           GACGGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                           dв.
                                                                              1 TCTAGAAATATAGCCGATACCAATTTTTCCACATGGACTTCCTTTATTCCAAAAGTCA
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            NI16; transgenic; herbicide resistance; mouse-ear cress; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule comprising Arabidopsis N116 promoter, useful in regulating transcription of coding sequence of
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                                    DB 13; Length 544;
                                                         Indels
              C; 95 G; 156 T; 0 U; 0 Other;
                                  Score 272.4; DB 13;
Pred. No. 1.6e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                                                       TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana NI16 promoter DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 12; SEQ ID NO 25; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawton
                                                                                                                                                                                                                                                                                                                                       ADR16844 standard; DNA; 862 BP
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11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00733685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2004; 2004US-00800161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-2004; 2004US-00760752
                                  99.4%;
Local Similarity 99.6%;
hes 273; Conservative
                 BP; 209 A; 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-580223/56.
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                 Sequence 544
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                                                                                                                                                                                          391
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                                     Query Match
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ADR16844
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                                                                                                                                ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                               697
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                                                                                                                                                                                                                          698 CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
                                                                                                                                                                                                                                                                                 121 CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                181 GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                                                                                                                1 TCTAGAAATATAGCCGATACCAATTTTTCCACACGACGACTTCCTTTATTCCAAAAGTCA
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Systemic acquired resistance, disease-resistance, transgenic plant, plant, NI16; NIM1 interactor; promoter; ds.
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707. .712
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0
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/*tag= a
/*note= "This promoter is specifically claimed"
365. .374
Length 862;
                                1; Indels
                                                                                                                                                                                                                                                                                                                                                  818 TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 851
                                                                                                                                                                                                                                                                                                                                   241 TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
   Score 272.4; DB 1
Pred. No. 1.8e-63;
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/note= "HEXAMERAT ·4 element"
                                    0; Mismatches
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/note= "MYCATR22 element"
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/note= "TCAI motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "TCAI motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana NI16 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= f
/note= "PAL BOX"
757. .762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2004; 2004US-00760752
   99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADV66225 standard; DNA; 862
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                                  Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
   Query Match
Best Local Similarity
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in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica. Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The present sequence is Arabidopsis thaliana NI16 promoter DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTGATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to an Arabidopsis NI16 gene promoter useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGGCTATAAGAGTTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
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                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NI16; SAR; systemic acquired resistance; mouse-ear cress; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 962 BP; 379 A; 125 C; 165 G; 293 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 272.4; DB 13; Length
Best Local Similarity 99.6%; Pred. No. 1.8e-63;
Matches 273; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrgacraagcrraaacgacgccgrraacarrrrc 951
                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 24; 39pp; English.
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/*tag= a
/note= "TCA1 motif"
/*tag= b
/note= "TCA1 motif"
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                                                                                                                 ģ.
                                                                                                                                                           Lawton KA;
                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS
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  15-DEC-1999; 99US-0171008P.
11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00738685.
20-JAN-2004; 2004US-00760752.
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99US-0171008P
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                                                                                                                                                           Cade RM, Dietrich RA,
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                                                                                                                                                                                                                                                                                               interest
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                                                                                                                                                                                                                                                                                                                                     The invention relates to a NI16 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression of SAR genes such as pathogenesis related protein (PR-1), thus allows broadspectrum disease resistance in plant such as resistance against spectrum disease resistance in plant such as resistance against beaudomonas syringae. The present sequence is the Arabidopsis thaliana NI16 gene including 5' upstream promoter. Note: This sequence is not given separately, but has been created from the NI16 gene (ADV66204) given in the sequence listing and the information provided in claim 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGCCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 TCTAAAAATATAGCCGATACCAATTTTTCCACACGTGGACTTCCTTATTCCAAAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAAGTGTGACGTCATGATACTTACGCTTTAAAAACATCGCATGATGATGTCATTAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NI16; transgenic; herbicide resistance; mouse-ear cress; promoter;
                                                                                                                                                                                                     Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 272.4; DB 14; Length 862; Pred. No. 1.8e-63; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 862 BP; 337 A; 112 C; 152 G; 261 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGACIAAGCITAAACGACGCCGITAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rrgacraagcrraaacgacgccrraacarrrrc 851
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                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                               Claim 1; Page; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2004; 2004US-00800161
    08-DEC-2000; 2000US-00733685
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Best Local Similarity 99.6%;
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR16843 standard; DNA; 962
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                                                                                            Cade RM, Dietrich RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                    WPI; 2005-020569/02.
P-PSDB; ADV66203.
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Length 962;

797

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     ADR16822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        817
                                                                                                                                                                                                                                                              New NI16 nucleic acid sequence and encoded protein, useful for increasing systemic acquired resistance gene expression in a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                       637
                                                                                                                                                                                                                                                                                                                                                                                                                                                        697
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                    578 TCTAAAATATAGCGGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Arabidopsis NII6 gene encoding a protein involved in the regulation of SAR gene expression in plants. The NII6 nucleic acid molecule and the encoded protein is useful in increasing systemic acquired resistance (SAR) gene expression in a plant. The present sequence is Arabidopsis thaliana NII6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGATGATAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                       salicylic acid response element"
                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 1700;
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                                                                                                       /*tag= g
/product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                                       Sequence 1700 BP; 593 A; 237 C; 361 G; 509 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGACIAAGCIIAAACGACGCCGIIAACAITIIC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2e-63;
                                                                              /*tag= f
/note= "HEXAMERAT 4 element"
863. .1231
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 272.4;
        *tag= c
note= "MYCATR22 element"
                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 3; 29pp; English.
                                                                                                                                                                                                        (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                 *tag= d
note= "CAMV AS1
                                                        '*tag= e
'note= "PAL box"
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.6%;
Matches 273; Conservative C
                                                                                                                                                                               15-DEC-1999; 99US-0171008P.
                                                                                                                                                                08-DEC-2000; 2000US-00733685
                                               .712
                                                                       .762
 .614
                        .665
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                                               misc_feature
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misc_feature
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The present invention relates to an Arabidopsis NII6 gene promoter useful in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica. Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The present sequence is Arabidopsis thaliana NII6 genomic DNA, including the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                           NI16; transgenic; herbicide resistance; mouse-ear cress; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3= d
3= "CAMV AS1 salicylic acid response element"
.712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity 99.4%; Score 272.4; DB 13; Length 1700; Similarity 99.6%; Pred. No. 2e-63; 73; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1700 BP; 593 A; 237 C; 361 G; 509 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "HEXAMERAT 4 element"
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/note= "MYCATR22 element"
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Arabidopsis thaliana NI16 genomic DNA
                                                                                                                                                                                                        /*tag= a
/note= "TCAl motif"
126. .435
                                                                                                                                                    Location/Qualifiers 365. .374
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/note= "TCA1 motif"
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/note= "PAL BOX"
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11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00735685.
20-JAN-2004; 2004US-00760752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'upstream promoter sequence
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                     Arabidopsis thaliana
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P-PSDB; ADR16821
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Gaps

1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA 60

Matches 273; Conservative

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ADR16822 ID ADR16822 Btandard; DNA; 1700 BP.

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The invention relates to a NI16 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression is spectrum disease resistance in plant such as resistance against Pseudomonas syringae. The present sequence is the Arabidopsis thaliana NI16 gene including 5' upstream promoter. Note: The promoter is specifically claimed in claim 1 - the isolated promoter is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTAGAAATATAGCCGATACCAATTTTTCCACACGATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                             Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 1700;
                                                                                                                                                                                                                                                                                                                                                 Sequence 1700 BP; 593 A; 237 C; 361 G; 509 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGACTAAGCTTAAACGACGCCGTTAACATTTTC 851
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                                                                                                                                                                                                                                                                                                                                                                              Score 272.4; DB Pred. No. 2e-63;
                                                                                                                                                                                                                                                                                                                                                                    99.4%; Scur. No. zc. 99.6%; Pred. No. zc. o; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. thaliana NIMIN-2 promoter SEQ ID NO:2.
                                                                                                                                            Example 3; SEQ ID NO 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                              Matches 273; Conservative
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    Dietrich RA;
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                                 2005-020569/02.
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                 P-PSDB; ADV66203
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    Cade RM,
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                   637
                                                120
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                                                                                                                                                                         GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
                                                                                                                                                                                                       GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 817
CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT
                                                                                                                                         CAATCTCCACCGTCCAATTTAATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Systemic acquired resistance; disease-resistance; transgenic plant; plant; NI16; NIM1 interactor; gene; ds.
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note= "CAMV AS1 salicylic acid response element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                      274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      '*tag= g
'note= "HEXAMERAT 4 element"
                                                                                                                                                                                                                                      TIGACTAAGCTTAAACGACGCCGTTAACATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "MYCATR22 element'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165. .374
/*tag= b
/note= "TCAI motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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note= "TCAI motif"
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note= "PAL BOX"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana NI16 gene.
                                                                                                                                                                                                                                                                                                                                                 ADV66204 standard; DNA; 1700
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note= "This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1231
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004248303-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                               ADV66204;
                                                                               638
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                                                                                                                                          698
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                                                                                                                                                                                                       758
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                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enhancer
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(SYGN ) SYNGENTA PARTICIPATIONS AG
                                               WPI; 2004-313378/29
                                                           P-PSDB; ADN17258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004154051-A1
                                                                                                                                                                                                                                                                                                                                                                21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cade RM,
                                                                                                                                                                                                                                                                                                                                             ADR16820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interest
                           Cad RM,
                                                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                      ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 1086
                                                                                                                                                                                                                                                                                                                                               1087 CAATCTCCACCGTCCAATTATTAAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC 1146
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                               Novel nucleic acid containing selectively inducible NIMIN-1 promoter sequence or NIMIN-2 promoter sequence, useful in controlled expression of desired expression products in suitable host expression organisms such as
                                                                                                         The invention relates to a novel nucleic acid (I) containing at least a first nucleotide sequence chosen from a NIMIN-1 promoter sequence of (ADW12660) and NIMIN-2 promoter sequence of (ADW12661), and its biologically active derivative. The polynucleotide of the invention is useful in controlled expression of desired expression products in suitable host expression organisms such as transgenic plants. The present sequence represents the NIMIN-2 promoter.
                                                                                                                                                                                                                                                                                                                                    CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                                                                                                                                                                                           GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
                                                                                                                                                                                                                                                                                            ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTTAGCAT 120
                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                     TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        systemic acquired resistance; mouse-ear cress; gene; ss.
                                                                                                                                                                                                           Score 258.4; DB 14; Length 1226;
Pred. No. 1.1e-59;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                          Sequence 1226 BP; 496 A; 146 C; 201 G; 383 T; 0 U; 0 Other;
                                                                                         Claim 1; SEQ ID NO 2; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGACTAAGCTTAAACGACG 1226
                                                                                                                                                                                                                                                                                                                                                                                                                    TTGACTAAGCTTAAACGACG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana NI16 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1999; 99US-0171008P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN17257 standard; cDNA; 509
                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
 Pfitzner A, Roth B;
                    WPI; 2005-114423/13
                                                                       transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6706952-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI16; SAR;
                                                                                                                                                                                                                                                                                                                 1027
                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN17257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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New NI16 nucleic acid sequence and encoded protein, useful for increasing systemic acquired resistance gene expression in a plant.
                                                                                                                                                                                                                                                                                                                             The invention relates to Arabidopsis NI16 gene encoding a protein involved in the regulation of SAR gene expression in plants. The NI16 mucleic acid molecule and the encoded protein is useful in increasing systemic acquired resistance (SAR) gene expression in a plant. The present sequence is Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NI16; transgenic; herbicide resistance; mouse-ear cress; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.3%; Score 52.8; DB 12; Length 509;
Best Local Similarity 96.4%; Pred. No. 0.00021;
Matches 54; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 509 BP; 158 A; 82 C; 133 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1; 39pp; English
                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
68. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawton KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1999; 99US-0171008P.
11-JAN-2000; 2000US-017519P.
08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2004; 2004US-00800161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR16820 standard; cDNA; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Dietrich RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-580223/56.
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The invention relates to a NI16 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression of SAR genes such as pathogenesis-related protein (PR-1), thus allows broad-spectrum disease resistance in plant such as resistance against Pseudomonas syringae. The present sequence is the Arabidopsis thaliana NI16 cDNA obtained via a NIMI two-hybrid screen.
                             in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica,
present invention relates to an Arabidopsis NI16 gene promoter useful
                                                                                                                 Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The
                                                                                                                                                                                                                                                                                                                                                                                                      CTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAATCAGCAAATAAACTTTTCTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Systemic acquired resistance; disease-resistance; transgenic plant; plant; NI16; NIM1 interactor; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                                                                                                                                                                        °,
                                                                                                                                                                                                                                                                                 DB 13; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Arabidopsis thaliana NI16 protein"
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                                                                                                                                                                                                                   Sequence 509 BP; 158 A; 82 C; 133 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                  present sequence is Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                                                       0.00021;
                                                                                                                                                                                                                                                                             Score 52.8; DB Pred. No. 0.000 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 1; 32pp; English
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68. .436
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                             19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADV66202 standard; cDNA; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2004; 2004US-00760752
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                                                                                                                                                                                                                                                                                                                                                                                                            AAAATCAGCAAATAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                           54; Conservative
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                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                              Matches
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   The
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DB 14; Length 509;

19.3%; Score 52.8;

Query Match

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type of a a coronary artery endothellum, umbilical artery or vein endothellum, cartery endothellum, umbilical artery or vein endothellum, cartery endothellum, pulmonary artery endothellum, prometry epithellum, prometry prosected epithellum, prometrial pepthellum, mammary epithellum, prosected epithellum, renal epithellum, renal prothellum, renal prothellum, renal problast, pulmonary artery smooth cuscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, cornic smooth muscle, mesangial cells, coronary artery smooth muscle, cortic smooth muscle, used properly as a smooth muscle, cortic smooth muscle, userine smooth muscle, astrocytes, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, skeletal muscle, astrocytes, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, press the certaining the level of RNA expression for a sample, determining the copy and distinguishing cell types. The gene or a protein certain and containing the level of company artery supplemental coronary artery and stages and praged to tumour type and stages.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
gene expression; gene; ss.
                                                                      219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                           Gaps
                                                                                                       1 AAATCAGCAATAAACTTTTCTTGACTAAGCTTAAACGACGCGGTAAACATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                         Human gene expression profile polynucleotide SEQ ID NO 676.
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 321 BP; 112 A; 51 C; 40 G; 113 T; 0 U; 5 Other;
  Pred. No. 0.00021;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%; Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 799; 850pp; English.
                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                               ABZ35565 standard; cDNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2002; 2002WO-US008456
96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2001; 2001US-0276947P
                                                                                                                                                                                                                                                                                                                                              (first entry)
                           54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-740862/80.
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antifungal agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200274979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                 ABZ35565;
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                           Matches
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The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polymucleotides, or immunogenic portions of the proteins. The ovarian tumour polymucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer prospession. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AASS1820-AASS531 and AASS5328-AASS5549
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                                                                                                                      64 agaagacraraacagaaarcararrraararraraaraarraaarraaracrrcaaararrrrca 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding ovarian tumor proteins, useful for treating ovarian cancer, and as probes, primers, and markers of cancer
                                                                                    4 inanatriccarricaaggrafitaritrarridcagcrcarcritaagrgacaaaariccarac 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
                                                     120 TCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
                                                                                                                                                                                                                                                                                                                                                               . `_
                    Gaps
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Pred. No. 0.085;
0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian PCR-subtracted cDNA library clone #1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 376; 378pp; English
                                                                                                                                                                                                                                                                                                                        AAS25538 standard; cDNA; 229 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2001; 2001WO-US003733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180403P
28-MAR-2000; 2000US-0192745P
 Best Local Similarity 56.7%;
Matches 76; Conservative
                                                                                                                                                                                                                      124 CATTANGATGATTA 137
                                                                                                                                                                                              240 CTTGACTAAGCTTA 253
                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Algate PA, Mannion J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progression.
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AAS25538/c
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163 GACTATAACAGAAATCATATTAATATTAAAATTAATACTTCAAATATCTTTCACATT 104
                          223 Triccarridaaggrafrafritarrificagcrcafcrraagrgacaaaarrccaracada 164
TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGAC
                                                                                                                                                                                                         Search completed: January 12, 2006, 00:32:55 Job time : 502 secs
                                                                                                                            244 ACTAAGCTTA 253
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15.3%; Score 42; DB 4; Length 229; 57.7%; Pred. No. 0.15; tive 0; Mismatches 55; Indels

Best Local Similarity 57.7 Matches 75; Conservative

Query Match

Sequence 229 BP; 96 A; 26 C; 33 G; 74 T; 0 U; 0 Other;

represent human ovarian tumour protein cDNA clones

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